



SEQUENCE LISTING

<10> Falco, Saverio Carl
Famodu, Layo
Rafalski, Jan A.
Ramaker, Michael
Tarczynski, Mitchell C.
Thorpe, Catherine

<120> PLANT METHIONINE SYNTHASE GENE AND METHODS FOR INCREASING THE
METHIONINE CONTENT OF THE SEEDS OF PLANTS

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 Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Ser
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 Ala Tyr Ala Glu Leu Glu Ser Ser Phe Ser Gly Leu Asn Val Leu Ile
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 Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Ser Tyr Lys Thr Leu Thr
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 Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
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Arg Tyr Asn Trp Ala Gly Gly Glu Ile Ala Phe Asp Thr Tyr Phe Ser
          85              90              95

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Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
 100 105 110
 Phe Asp Thr Asn Tyr His Phe Ile Val Pro Glu Leu Gly Pro Asp Val
 115 120 125
 Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asp Glu Tyr Lys Glu Ala
 130 135 140
 Lys Gly Leu Gly Val Asp Thr Val Pro Val Leu Ile Gly Pro Val Ser
 145 150 155 160
 Tyr Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Ser Phe Pro
 165 170 175
 Leu Leu Ser Leu Leu Asp Lys Val Leu Pro Ile Tyr Lys Glu Val Ile
 180 185 190
 Ala Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
 195 200 205
 Thr Leu Val Leu Asp Leu Gln Ala His Gln Leu Glu Ala Phe Thr Lys
 210 215 220
 Ala Tyr Ala Glu Leu Glu Ser Ser Leu Ser Gly Leu Asn Val Leu Thr
 225 230 235 240
 Glu Thr Tyr Phe Ala Asp Val Pro Ala Glu Ala Phe Lys Thr Leu Thr
 245 250 255
 Ala Leu Lys Gly Val Thr Ala Phe Gly Phe Asp Leu Val Arg Gly Ala
 260 265 270
 Gln Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
 275 280 285
 Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
 290 295 300
 Ala Ser Leu Asn Leu Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
 305 310 315 320
 Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
 325 330 335
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 Ala Gly His Lys Asp Glu Ala Phe Phe Ser Ala Asn Ala Thr Ala Gln
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 Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Glu Ala Val Gln Lys
 385 390 395 400
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 405 410 415
 Ser Ser Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
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Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Val Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Glu Glu Tyr Val
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Lys Ala Ile Lys Ala Glu Ile Lys Lys Val Val Asp Leu Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495

Val Glu Tyr Phe Gly Glu Gln Leu Ser Gly Phe Ala Phe Thr Ala Asn
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Gly Trp Val Gln Ser Tyr Gly Ser Arg Cys Val Lys Pro Pro Ile Ile
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Tyr Gly Asp Val Ser Arg Pro Asn Pro Met Thr Val Phe Trp Ser Lys
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Thr Ala Gln Ser Met Thr Lys Arg Pro Met Lys Gly Met Leu Thr Gly
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Pro Val Thr Ile Leu Asn Trp Ser Phe Val Arg Asn Asp Gln Pro Arg
565 570 575

Phe Glu Thr Cys Tyr Gln Ile Ala Leu Ala Ile Lys Asp Glu Val Glu
580 585 590

Asp Leu Glu Lys Ala Gly Ile Thr Val Ile Gln Ile Asp Glu Ala Ala
595 600 605

Leu Arg Glu Gly Leu Pro Leu Arg Lys Ala Glu His Ala Phe Tyr Leu
610 615 620

Asn Trp Ala Val His Ser Phe Arg Ile Thr Asn Val Gly Ile Gln Asp
625 630 635 640

Thr Thr Gln Ile His Thr His Met Cys Tyr Ser Asn Phe Asn Asp Ile
645 650 655

Ile His Ser Ile Ile Asp Met Asp Ala Asp Val Ile Thr Ile Glu Asn
660 665 670

Ser Arg Ser Asp Glu Lys Leu Leu Ser Val Phe Arg Glu Gly Val Lys
675 680 685

Tyr Gly Ala Gly Ile Gly Pro Gly Val Tyr Asp Ile His Ser Pro Arg
690 695 700

Ile Pro Ser Thr Glu Glu Ile Ala Asp Arg Val Asn Lys Met Leu Ala
705 710 715 720

Val Leu Asp Thr Asn Ile Leu Trp Val Asn Pro Asp Cys Gly Leu Lys
725 730 735

Thr Arg Lys Tyr Ala Glu Val Lys Pro Ala Leu Glu Asn Met Val Ser
740 745 750

Ala Ala Lys Ala Ile Arg Thr Gln Leu Ala Ser Ser Lys
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 agctcaagtt tgccttggag tctttctggg atgggaagag cagcgctgag gatttggaga 180
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 <213> Triticum aestivum

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 Asp Leu Glu Lys Val Ala Ala Asp Leu Arg Ala Ser Ile Trp Lys Gln
 35 40 45
 Met Ser Glu Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
 50 55 60

Tyr Asp Gln Val Leu Asp Thr Thr Ala Met Leu Gly Ala Val Pro Asp
 65 70 75 80
 Arg Tyr Ser Trp Thr Gly Gly Glu Ile Gly His Ser Thr Tyr Phe Ser
 85 90 95
 Met Xaa Lys Gly Asn Ala Thr Val Pro Ala Met Glu Met Thr Lys Trp
 100 105 110
 Phe Asp Thr Asn Xaa His Phe Xaa Val Pro Glu Leu
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gggtccgccc tgagtacaag gcgaaagaag atctctgang aggagtatgt cagtgtctatc 240
aaggaagaaa ttancaaagg ttgtcaagat tcaaagagga gcttgacatt gatgttctcn 300
tccaatggag aagcctgana aaaatgacat nggtnaanta ctccggcnan caaattatcn 360
gggtttgcaa ttactgccaa tggatgggtg caatcctatg gattacttgc gtnaancacc 420
gatnatchat gggatgtaan cgccaaccc atganatctt ctgggtcaana tgntcaggac 480
atanccctccc ccaatgaagg aatntnacgg cctttaaatc ccaacnggct ttntnagaac 540
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atcagngtca atnatagggg ccaaaagg 628

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<213> Triticum aestivum

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<222> (116)

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Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Ile Leu Pro Thr Thr Thr
35 40 45

Ile Gly Ser Phe Pro Gln Thr Met Asp Leu Arg Arg Val Arg Arg Glu
50 55 60

Tyr Lys Ala Lys Glu Asp Leu Xaa Xaa Gly Val Cys Gln Cys Tyr Gln
65 70 75 80

Gly Arg Asn Xaa Gln Arg Leu Ser Arg Phe Lys Glu Glu Leu Asp Ile
85 90 95

Asp Val Leu Xaa Gln Trp Arg Ser Leu Xaa Lys Met Thr Xaa Val Xaa
100 105 110

Tyr Phe Gly Xaa Gln Ile
115

<210> 11

<211> 765

<212> PRT

<213> Catharanthus roseus

<400> 11

Met Ala Ser His Ile Val Gly Tyr Pro Arg Met Gly Pro Lys Arg Glu
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Leu Lys Phe Ala Leu Glu Ser Phe Trp Asp Lys Lys Ser Ser Ala Glu
20 25 30

Asp Leu Gln Lys Val Ala Ala Asp Leu Arg Ser Ser Ile Trp Lys Gln
35 40 45

Met Ala Asp Ala Gly Ile Lys Tyr Ile Pro Ser Asn Thr Phe Ser Tyr
50 55 60

Tyr Asp Gln Val Leu Asp Thr Ala Thr Met Leu Gly Ala Val Pro Pro
65 70 75 80

Arg Tyr Asn Phe Ala Gly Gly Glu Ile Gly Phe Asp Thr Tyr Phe Ser
85 90 95

Met Ala Arg Gly Asn Ala Ser Val Pro Ala Met Glu Met Thr Lys Trp
100 105 110

Phe Asp Thr Asn Tyr His Tyr Ile Val Pro Glu Leu Gly Pro Glu Val
115 120 125

Asn Phe Ser Tyr Ala Ser His Lys Ala Val Asn Glu Tyr Lys Glu Ala
130 135 140

Lys Glu Leu Gly Val Asp Thr Val Pro Val Leu Val Gly Pro Val Thr
145 150 155 160

Phe Leu Leu Leu Ser Lys Pro Ala Lys Gly Val Glu Lys Thr Phe Pro
165 170 175

Leu Leu Ser Leu Leu Asp Lys Ile Leu Pro Val Tyr Lys Glu Val Ile
180 185 190

Gly Glu Leu Lys Ala Ala Gly Ala Ser Trp Ile Gln Phe Asp Glu Pro
195 200 205

Thr Leu Val Leu Asp Leu Glu Ser His Gln Leu Glu Ala Phe Thr Lys
210 215 220

Ala Tyr Ser Glu Leu Glu Ser Thr Leu Ser Gly Leu Asn Val Ile Val
225 230 235 240

Glu Thr Tyr Phe Ala Asp Ile Pro Ala Glu Thr Tyr Lys Ile Leu Thr
245 250 255

Ala Leu Lys Gly Val Thr Gly Phe Gly Phe Asp Leu Val Arg Gly Ala
260 265 270

Lys Thr Leu Asp Leu Ile Lys Gly Gly Phe Pro Ser Gly Lys Tyr Leu
275 280 285

Phe Ala Gly Val Val Asp Gly Arg Asn Ile Trp Ala Asn Asp Leu Ala
290 295 300

Ala Ser Leu Ser Thr Leu Gln Ser Leu Glu Gly Ile Val Gly Lys Asp
305 310 315 320

Lys Leu Val Val Ser Thr Ser Cys Ser Leu Leu His Thr Ala Val Asp
325 330 335

Leu Val Asn Glu Pro Lys Leu Asp Lys Glu Ile Lys Ser Trp Leu Ala
340 345 350

Phe Ala Ala Gln Lys Val Val Glu Val Asn Ala Leu Ala Lys Ala Leu
355 360 365

Ala Gly Glu Lys Asp Glu Ala Phe Phe Ser Glu Asn Ala Ala Ala Gln
370 375 380

Ala Ser Arg Lys Ser Ser Pro Arg Val Thr Asn Gln Ala Val Gln Lys
385 390 395 400

Ala Ala Ala Ala Leu Arg Gly Ser Asp His Arg Arg Ala Thr Thr Val
405 410 415

Ser Ala Arg Leu Asp Ala Gln Gln Lys Lys Leu Asn Leu Pro Val Leu
420 425 430

Pro Thr Thr Thr Ile Gly Ser Phe Pro Gln Thr Leu Glu Leu Arg Arg
435 440 445

Val Arg Arg Glu Tyr Lys Ala Lys Lys Ile Ser Glu Asp Asp Tyr Val
450 455 460

Lys Ala Ile Lys Glu Glu Ile Ser Lys Val Val Lys Leu Gln Glu Glu
465 470 475 480

Leu Asp Ile Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met
485 490 495


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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<210> 14
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 14
ctcacggtcc gatgagaagc tcct 24

<210> 15
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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<210> 16
<211> 1638
<212> DNA
<213> Zea mays

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gtccgcctcc gcggcggcgg atgtcagcgc aattcctaac gctaagggtg cgcagccgtc 240
cgccgtcgta ttggccgagc gtaacctgct cggtccgac gccagcctcg ccgtccacgc 300
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tatccgtcaa attcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1620
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<212>	PRT
<213>	Zea mays

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Arg Ser Leu Arg Arg Arg Ser Ser Pro Pro Ser Pro Ala Ala Pro Trp
35 40 45

Pro Leu Pro Pro Ser Ser Ala Ser Arg Gln Thr Ser Ser Ala Ser Ala
50 55 60

Ala Ala Asp Val Ser Ala Ile Pro Asn Ala Lys Val Ala Gln Pro Ser
65 70 75 80

Ala Val Val Leu Ala Glu Arg Asn Leu Leu Gly Ser Asp Ala Ser Leu
85 90 95

Ala Val His Ala Gly Glu Arg Leu Gly Arg Arg Ile Ala Thr Asp Ala
100 105 110

Ile Thr Thr Pro Val Val Asn Thr Ser Ala Tyr Trp Phe Asn Asn Ser
115 120 125

Gln Glu Leu Ile Asp Phe Lys Glu Gly Arg His Ala Ser Phe Glu Tyr
130 135 140

Gly Arg Tyr Gly Asn Pro Thr Thr Glu Ala Leu Glu Lys Lys Met Ser
145 150 155 160

Ala Leu Glu Lys Ala Glu Ser Thr Val Phe Val Ala Ser Gly Met Tyr
165 170 175

Ala Ala Val Ala Met Leu Ser Ala Leu Val Pro Ala Gly Gly His Ile
180 185 190

Val Thr Thr Thr Asp Cys Tyr Arg Lys Thr Arg Ile Tyr Met Glu Asn
195 200 205

Glu Leu Pro Lys Arg Gly Ile Ser Met Thr Val Ile Arg Pro Ala Asp
210 215 220

Met Asp Ala Leu Gln Asn Ala Leu Asp Asn Asn Val Ser Leu Phe
225 230 235 240

Phe Thr Glu Thr Pro Thr Asn Pro Phe Leu Arg Cys Ile Asp Ile Glu
245 250 255

His Val Ser Asn Met Cys His Ser Lys Gly Ala Leu Leu Cys Ile Asp
260 265 270

Ser Thr Phe Ala Ser Pro Ile Asn Gln Lys Ala Leu Thr Leu Gly Ala
275 280 285


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 <212> PRT
 <213> Zea mays

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 35 40 45
 Val Ala Gln Ile Val Ala Ala Ala Trp Ser Asp Cys Pro Ala Ala Arg
 50 55 60
 Pro His Leu Gly Gly Gly Gly Arg Arg Ala Arg Gly Val Ala Ser Ser
 65 70 75 80
 His Ala Ala Ala Ala Ser Ala Ala Ala Ala Ala Ser Ala Ala Ala Glu
 85 90 95

<210> 23
<211> 449
<212> PRT
<213> Escherichia coli

<400> 23
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Phe Asp Ala Met Asn Arg Ser Ala Asp Ile Val Leu Ser Asp Ala Asn
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Val Arg Leu Val Val Leu Ser Ala Ser Ala Gly Ile Thr Asn Leu Leu
35 40 45
Val Ala Leu Ala Glu Gly Leu Glu Pro Gly Glu Arg Phe Glu Lys Leu
50 55 60
Asp Ala Ile Arg Asn Ile Gln Phe Ala Ile Leu Glu Arg Leu Arg Tyr
65 70 75 80
Pro Asn Val Ile Arg Glu Glu Ile Glu Arg Leu Leu Glu Asn Ile Thr
85 90 95
Val Leu Ala Glu Ala Ala Ala Leu Ala Thr Ser Pro Ala Leu Thr Asp
100 105 110
Glu Leu Val Ser His Gly Glu Leu Met Ser Thr Leu Leu Phe Val Glu
115 120 125
Ile Leu Arg Glu Arg Asp Val Gln Ala Gln Trp Phe Asp Val Arg Lys
130 135 140
Val Met Arg Thr Asn Asp Arg Phe Gly Arg Ala Glu Pro Asp Ile Ala
145 150 155 160
Ala Leu Ala Glu Leu Ala Ala Leu Gln Leu Leu Pro Arg Leu Asn Glu
165 170 175
Gly Leu Val Ile Thr Gln Gly Phe Ile Gly Ser Glu Asn Lys Gly Arg
180 185 190
Thr Thr Thr Leu Gly Arg Gly Gly Ser Asp Tyr Thr Ala Ala Leu Leu
195 200 205
Ala Glu Ala Leu His Ala Ser Arg Val Asp Ile Trp Thr Asp Val Pro
210 215 220
Gly Ile Tyr Thr Thr Asp Pro Arg Val Val Ser Ala Ala Lys Arg Ile
225 230 235 240
Asp Glu Ile Ala Phe Ala Glu Ala Ala Glu Met Ala Thr Phe Gly Ala
245 250 255
Lys Val Leu His Pro Ala Thr Leu Leu Pro Ala Val Arg Ser Asp Ile
260 265 270
Pro Val Phe Val Gly Ser Ser Lys Asp Pro Arg Ala Gly Gly Thr Leu
275 280 285

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Val Cys Asn Lys Thr Glu Asn Pro Pro Leu Phe Arg Ala Leu Ala Leu
 290                               295                   300

Arg Arg Asn Gln Thr Leu Leu Thr Leu His Ser Leu Asn Met Leu His
 305                               310                   315                   320

Ser Arg Gly Phe Leu Ala Glu Val Phe Gly Ile Leu Ala Arg His Asn
                               325                   330                   335

Ile Ser Val Asp Leu Ile Thr Thr Ser Glu Val Ser Val Ala Leu Thr
                               340                   345                   350

Leu Asp Thr Thr Gly Ser Thr Ser Thr Gly Asp Thr Leu Leu Thr Gln
                               355                   360                   365

Ser Leu Leu Met Glu Leu Ser Ala Leu Cys Arg Val Glu Val Glu Glu
 370                               375                   380

Gly Leu Ala Leu Val Ala Leu Ile Gly Asn Asp Leu Ser Lys Ala Cys
 385                               390                   395                   400

Ala Val Gly Lys Glu Val Phe Gly Val Leu Glu Pro Phe Asn Ile Arg
                               405                   410                   415

Met Ile Cys Tyr Gly Ala Ser Ser His Asn Leu Cys Phe Leu Val Pro
                               420                   425                   430

Gly Glu Asp Ala Glu Gln Val Val Gln Lys Leu His Ser Asn Leu Phe
 435                               440                   445

```

Glu

```

<210> 24
<211> 36
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

```

```

<400> 24
gatccatggc tgaaattggt gtctccaaat ttggcg                                     36

```

```

<210> 25
<211> 36
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

```

```

<400> 25
gtaccgcaa atttggagac aacaatttca gccatg                                     36

```

```

<210> 26
<211> 30
<212> DNA
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

```

```

<400> 26
atggcagcca agatgcttgc attgttcgct                                     30

<210> 27
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 27
gaatgcagca ccaacaaagg gttgctgtaa                                     30

<210> 28
<211> 2123
<212> DNA
<213> Zea mays

<400> 28
tctagagcct attaccatct ctactcacgg gtcgtagagg tggtagaggta ggctacagct      60
ggtgacaatc ctactcaccc tttgtaatcc tctacggctc tacgcgtagt taattgggta      120
gatgtcaacc ccctctctaa gtggcagtag tgggcttggt tatacctgct agtgcctggg      180
gatgttctat ttttctagta gtgcttgatc aaacattgca tagtttgact tgggacaaac      240
tgtctgatat atatatatat ttttgggcag agggagcagt aagaacttat ttagaaatgt      300
aatcatttgt taaaaaagggt ttaattttgc tgctttcttt cgtaaatgtt gttttcacat      360
tagattttct ttgtgttata tacactggat acatacaaat tcagttgcag tagtctctta      420
atccacatca gctaggcata ctttagcaaa agcgaattac acaaactctag tgtgcctgtc      480
gtcacattct caataaaactc gtcattgttt actaaaagta ccttttcgaa gcatcatatt      540
aatccgaaaa cagttaggga agtctccaaa tctgaccaa tgccaagtca tcgtccagct      600
tatcagcatc caactttcag tttcgcattg gctagaaatt gtttttcatt tacattggcca      660
ttgttgactg catgcattct taaataggac cttagacgat aatcgcaatc gcataatccac      720
tattctctag gaagcaaggg aatcacatcg ccatggcagc caagatgttt gcattgtttg      780
cgctcctagc tctttgtgca accgccacta gtgctaccca tatcccaggg cacttgtcac      840
cactactgat gccattggct accatgaacc catggatgca gtactgcatg aagcaacagg      900
gggttgccaa cttgttagcg tggccgaccc tgatgctgca gcaactgttg gcctcacccg      960
ttcagcagtg ccagatgcc aatgatgatgc cgggtatgat gccaccgatg acgatgatgc     1020
cgatgccgag tatgatgcca tcgatgatgg tgccgactat gatgtcacca atgacgatgg     1080
ctagtatgat gccgccgatg atgatgccaa gcatgatttc accaatgacg atgccgagta     1140
tgatgccttc gatgataatg ccgaccatga tgtcaccaat gattatgccg agtatgatgc     1200
caccaatgat gatgccgagc atggtgtcac caatgatgat gccaaacatg atgacagtgc     1260
cacaatgtta ctctggttct atctcacaca ttatacaaca acaacaatta ccattcatgt     1320
tcagccccac agccatggcg atcccaccca tgttcttaca gcagcccttt gttgggtgctg     1380
cattctagat ctagatataa gcatttgtgt agtaccctaat aatgaagtcg gcattgccatc     1440
gcatacgact cattgttttag gaataaaaaca agctaataat gacttttctc tcattataac     1500
ttatatctct ccattgtctgt ttgtgtgttt gtaatgtctg ttaatcttag tagattatat     1560
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tagtttttaac catacctaga cattatgtat atataggcgg cttaacaaaa gctatgtact     1680
cagtaaaatc aaaacgactt acaattttaa atttagaaag tacattttta ttaatagact     1740
aggtgagtac ttgtgcgttg caacgggaac atataataac ataataactt atatacaaaa     1800
tgtatcttat attgttataa aaaatatctt ataattccatt tgtaatccta gtcatacata     1860
aattttgtta ttttaattta gttgtttcac tactacattg caaccattag tatcatgcag     1920
acttcgatat atgccaagat ttgcatggtc tcatcattga agagcacatg tcacacctgc     1980
cggtagaagt tctctcgtag attgtcagtc atcaggtacg caccaccata cagcgttgct     2040
taaacaaaaa aacaagtgtg tgtgtttgag aagagaatta agacaggcag acacaaaagt     2100
acccgacgat ggcgagtcgg tca                                     2123

<210> 29
<211> 211
<212> PRT
<213> Zea mays

```

<400> 29
Met Ala Ala Lys Met Phe Ala Leu Phe Ala Leu Leu Ala Leu Cys Ala
1 5 10 15
Thr Ala Thr Ser Ala Thr His Ile Pro Gly His Leu Ser Pro Leu Leu
20 25 30
Met Pro Leu Ala Thr Met Asn Pro Trp Met Gln Tyr Cys Met Lys Gln
35 40 45
Gln Gly Val Ala Asn Leu Leu Ala Trp Pro Thr Leu Met Leu Gln Gln
50 55 60
Leu Leu Ala Ser Pro Leu Gln Gln Cys Gln Met Pro Met Met Met Pro
65 70 75 80
Gly Met Met Pro Pro Met Thr Met Met Pro Met Pro Ser Met Met Pro
85 90 95
Ser Met Met Val Pro Thr Met Met Ser Pro Met Thr Met Ala Ser Met
100 105 110
Met Pro Pro Met Met Met Pro Ser Met Ile Ser Pro Met Thr Met Pro
115 120 125
Ser Met Met Pro Ser Met Ile Met Pro Thr Met Met Ser Pro Met Ile
130 135 140
Met Pro Ser Met Met Pro Pro Met Met Met Pro Ser Met Val Ser Pro
145 150 155 160
Met Met Met Pro Asn Met Met Thr Val Pro Gln Cys Tyr Ser Gly Ser
165 170 175
Ile Ser His Ile Ile Gln Gln Gln Gln Leu Pro Phe Met Phe Ser Pro
180 185 190
Thr Ala Met Ala Ile Pro Pro Met Phe Leu Gln Gln Pro Phe Val Gly
195 200 205
Ala Ala Phe
210

<210> 30
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 30
atgaaccctt ggatgca 17

<210> 31
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 31
cccacagcaa tggcgat 17

Ala Ala Phe
210

<210> 34
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 34
ctagcccggg tac 13

<210> 35
<211> 13
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 35
ctaggtaccc ggg 13

<210> 36
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 36
ccacttcacg acccatatcc cagggcactt 30

<210> 37
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 37
ttctatctag aatgcagcac caacaaaggg 30

<210> 38
<211> 579
<212> DNA
<213> Zea mays

<400> 38
tcatgaccca tatcccaggg cacttggtcac cactactgat gccattggct accatgaacc 60
cttggtatgca gtactgcatg aagcaacagg ggggttgccaa cttgttagcg tggccgaccc 120
tgatgctgca gcaactgttg gcctcaccgc ttcagcagtg ccagatgcca atgatgatgc 180
cgggtatgat gccaccgatg acgatgatgc cgatgccgag tatgatgcca tcgatgatgg 240
tgccgactat gatgtcacca atgacgatgg ctagtatgat gccgccgatg atgatgccaa 300
gcatgatttc accaatgacg atgccgagta tgatgccttc gatgataatg ccgaccatga 360
tgtcaccaat gattatgccg agtatgatgc caccaatgat gatgccgagc atgggtgtcac 420
caatgatgat gccaaacatg atgacagtgc cacaatgtta ctctggttct atctcacaca 480
ttatacaaca acaacaatta ccattcatgt tcagccccac agcaatggcg atccccacca 540
tgttcttaca gcagcccttt gttgggtgctg cattctaga 579

<210>	39
<211>	191
<212>	PRT
<213>	Zea mays

30

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<210> 42
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 42
gatcccatgg cgccccttaa gtccaccgcc agcctccccg tcgcccgcgc ctccct      55

<210> 43
<211> 55
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 43
ctagaggagc ggcgggagac ggggaggctg gcggtggact taaggggcgc catgg      55

<210> 44
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 44
catggcgccc accgtgatga tggcctcgtc ggccaccgcc gtcgctccgt tccaggggc 59

<210> 45
<211> 59
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 45
ttaagccctt ggaacggagc gacggcggtg gccgacgagg ccatcatcac ggtgggcgc 59

<210> 46
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 46
catggctggc ttccccacga ggaagaccaa caatgacatt acctccattg ctagcaacgg 60
tggaagagta caatg      75

<210> 47
<211> 75
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

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```

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 53
gaaaccatgg ccagtgtgat tgcgcaggca 30

<210> 54
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic oligonucleotide

<400> 54
gaaaggtacc ttacaacaac tgtgccagc 29

<210> 55
<211> 1494
<212> DNA
<213> Glycine max

<220>
<221> unsure
<222> (1461)

<220>
<221> unsure
<222> (1464)

<220>
<221> unsure
<222> (1465)

<400> 55
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ggatgaggtt ttcttttctg ctaatgctgc tgccttggct tcaaggaagt cctccccaag 120
ggtgataaat gaggtgtgcc aaaaagccgc tgctgctctg aagggtctctg atcatcgag 180
ggccacaaat gttagtgccg ggttggatgc tcaacagaag aaattgaatc tttctgttct 240
tccaacaact acaattggat ctttccctca aactgccgat cttagaagrg twcgycgtga 300
attcaaggct aacaagatct ccgaggaaga gtatgthaag tcaattaagg aggaaattcg 360
caaagtgtgt garcttcaag aagagcttga tattgatgtt cttgttcattg gagaaccaga 420
gagaaatgat atggttgagt acttcggtga rcaattgtca ggctttgcct tcacygttaa 480
tgggtgggtg caatcctatg gttcccgttg ygtgaagcca ccratcatct atggtgatgt 540
gagccgcccc aagccaatga cygtcttctg gtcattctctg gctcagagct ttaccaagcg 600
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ctgtggtctc aagaccgcga agtacactga agtgaagccc gccctcacia acatggttgc 1200
cgcagcaaaa ctcatccgta acgaacttgc caagtgaatg gtataagaaa gtagaatcta 1260
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tcaataaccg tgtgtggaat atttagatgt ttttagcatgc tctgtgagca attgattctt 1380
cctcaacccc tctcccctta ttttcccaa ctctgtttt ccctaataaa tggtgtatct 1440
ttgctttgcc gcaatcctta nttngatat gaaatattac cagttttgtg caaa 1494
  
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